

General Description References Links Keywords Sequence

**General information**www.uniprot.org **Q12563**Entry name **Q12563**Accession number **Q12563**

Created TrEMBLrel. 01, 1-NOV-1996

Sequence update TrEMBLrel. 01, 1-NOV-1996

Annotation update TrEMBLrel. 25, 1-OCT-2003

**Description and origin of the Protein**Description Alpha-mannosidase (EC 3.2.1.113).

Organism source Aspergillus phoenicis.

Taxonomy Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; Trichocomaceae; Aspergillus.

NCBI TaxID **5063****References**

[1] Inoue,T., Yoshida,T., Ichishima,E.,  
**Molecular cloning and nucleotide sequence of the 1,2-alpha-D- mannosidase gene of Aspergillus saitoi and expression of the gene in yeast cells.**  
(1995) *Biochim. Biophys. Acta* **1253**:141-145

Position SEQUENCE FROM N.A.

Medline **96106423**PubMed **8519794****Database cross-references**EMBL **D49827; BAA08634.1; -.**HSSP P31723; **1KRE**.**GO:0016020**; C:membrane; IEA.**GO:0005509**; F:calcium ion binding; IEA.GO **GO:0016798**; F:hydrolase activity, acting on glycosyl bonds; IEA.**GO:0004571**; F:mannosyl-oligosaccharide 1,2-alpha-mannosid...; IEA.**GO:0005975**; P:carbohydrate metabolism; IEA.**GO:0006487**; P:N-linked glycosylation; IEA.InterPro **IPR001382**; Glyco\_hydro\_47.Pfam **PF01532**; **Glyco\_hydro\_47**; 1.PRINTS **PR00747**; GLYHDRLASE47.ProDom **PD003239**; Glyco\_hydro\_47; 1.**Keywords****Glycosidase**; **Hydrolase**;**Sequence information**

Length: **513 aa**, molecular weight: **55874 Da**, CRC64 checksum: **0FDAB2CB27E93724**

MHLPSLSSL TALAIASPSA AYPHFGSSQP VLHSSSDTTQ SRADAIAAF SHAWDGYLQY	60
AFPHDELHPV SNGYGDSRNG WGASAVDALS TAVIMRNATI VNQILDHVVK IDYSKTNTV	120
SLFETTIRYL GGMLSGYDLL KGPVSDLVQN SSKIDVLLTQ SKNLADVLKF AFDTPSGVPY	180
NNLNITSGGN DGAKTNGLAV TGTLALEWTR LSDLTGDTTY ADLSQKAESY LLNPQPKSAE	240
PFPGLVGNSNI NISNGQFTDA QVSWNNGDDS YYEYLIKMYV YDPKRGFLYK DRWVAAAQST	300
MQHLASHPSS RPDLTFLASY NNGTLGLSSQ HLTCFDGGSF LLGGTVLNRT DFINFGLDLV	360
SGCHDTYNST LTGIGPESFS WDTSDIPSSQ QSLYEKAGFY ITSGAYILRP EVIESFYYAW	420
RVTGQETYRD WIWSAFSAVN DYCRTSSGFS GLTDVNAANG GSRYDNQESF LFAEVMKYSY	480
MAFAEDAAWQ VQPGSGNQFV FNTEAHPVRV SST	513

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